

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:19:49 ; Search time 38 Seconds
(without alignments)
346.887 Million cell updates/sec

Title: US-10-621-911A-2
Perfect score: 697
Sequence: 1 MNHTSQAFITTAASGQPPNY.....VVITVSVIIIVLNAQNLT 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	643	92.3	137	2 JC1241	beta-interferon-in
2	464	66.6	133	2 S17182	interferon-induced
3	449	64.4	132	2 S17183	interferon-induced
4	387	55.5	125	2 A31454	interferon-inducib
5	83.5	12.0	698	1 S00742	cytochrome-c oxida
6	83	11.9	722	2 AF1421	hypothetical membr
7	80	11.5	645	1 ODPPI	cytochrome-c oxida
8	80	11.5	645	1 S07751	cytochrome-c oxida
9	76.5	11.0	306	2 T09067	extensin-like prot
10	75	10.8	1810	2 T31092	probable voltage-g
11	73.5	10.5	412	2 A70839	probable membrane
12	72.5	10.4	84	2 S75757	hypothetical prote
13	72	10.3	254	2 S40702	hypothetical prote
14	72	10.3	449	2 H97249	protein containing
15	72	10.3	616	2 F90371	amino acid transpo
16	71.5	10.3	293	2 D70514	probable oxidoredu
17	71.5	10.3	722	2 AD1796	hypothetical membr
18	70.5	10.1	842	2 T04880	potassium transpor
19	70	10.0	389	1 S73933	prolipoprotein dia
20	70	10.0	537	2 G82873	conserved hypothet
21	70	10.0	1147	2 A82340	sensor histidine k
22	69.5	10.0	182	2 F88979	protein F37B4.1 [i
23	69.5	10.0	746	2 G02838	enhancer-of-zeste
24	69	9.9	408	2 B64708	glutamate permease
25	68.5	9.8	464	2 C69356	conserved hypothet
26	68.5	9.8	467	1 B4038	tryptophanase (EC
27	68.5	9.8	574	2 T41068	hypothetical prote
28	68	9.8	448	1 S24756	vicilin-like stora
29	67.5	9.7	352	2 H87236	probable integral

30	67.5	9.7	694	2 T33561	hypothetical prote
31	67	9.6	297	2 AH3649	iron(iii)-transpor
32	67	9.6	329	2 S73391	hypothetical prote
33	67	9.6	391	2 F86759	hypothetical prote
34	67	9.6	918	2 A88188	protein C18H9.3 [i
35	67	9.6	1918	2 S43719	lactase (EC 3.2.1.1
36	67	9.6	1920	2 S43721	lactase (EC 3.2.1.1
37	67	9.6	1926	2 S01169	beta-glycosidase c
38	66.5	9.5	958	2 S41013	hypothetical prote
39	66.5	9.5	1040	2 D88568	protein ZK757.3 [i
40	66	9.5	282	2 G75384	probable lipase -
41	66	9.5	310	2 T00709	syntaxin-related p
42	66	9.5	408	2 H71813	sodium/glutamate s
43	66	9.5	1249	2 F86909	probable DNA gyrase
44	66	9.5	1273	2 T10006	DNA topoisomerase
45	65.5	9.4	435	2 B83958	glucose-inhibited

ALIGNMENTS

RESULT 1

JC1241
beta-interferon-induced protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Mar-1995
C:Accession: JC1241; S16757
R:Hayzer, D.J.; Brinson, E.; Runge, M.S.
Gene 117, 277-278, 1992
A:Title: A rat beta-interferon-induced mRNA: Sequence characterization.
A:Reference number: JC1241; MUID:92347706; PMID:1639276
A:Accession: JC1241
A:Molecule type: mRNA
A:Residues: 1-137 <HAY>
A:Cross-references: GB:X61381
A:Experimental source: aortic smooth muscle
A>Note: The authors translated the codon GCG for residue 9 as Val, ACA for residue 10 as

Query Match 92.3%; Score 643; DB 2; Length 137;
Best Local Similarity 89.8%; Pred. No. 1.1e-60;
Matches 123; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY	1	MNHTSQAFITTAASGQPPNYERIKEEYEVAEMGAPHGSAVTRTTVINNPRESVDPDVWV	60
DB	1	MNHTSQAFITTAASGQPPNYERIKEEYEVAEMGAPHGSAVTRTTVINNPRESVDPDVWV	60
QY	61	SLFNTLPMFCLGFIAYAVSVKSRDRKMGVDTGAQAYASTAKCLNTSTLVSILMVVI	120
DB	61	SLFNTLPMFCLGFIAYAVSVKSRDRKMGVDTGAQAYASTAKCLNTSTLVSILMVVI	120
QY	121	TIVSVIIIVLNAQNLT	137
DB	121	TIVTVIIIALNAPRLQT	137

RESULT 2

S17182
interferon-induced protein 1-8U - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S17182
R:Lewin, A.R.; Reid, L.E.; McMahon, M.; Stark, G.R.; Kerr, I.M.
Eur. J. Biochem. 199, 417-423, 1991
A:Title: Molecular analysis of a human interferon-inducible gene family.
A:Reference number: S17182; MUID:91301153; PMID:1906403
A:Accession: S17182
A:Molecule type: DNA
A:Residues: 1-133 <LEW>
A:Cross-references: UNIPROT:Q01628; EMBL:X57352; NID:g311374; PID:CAA040626.1; PID:g2333

Query Match 66.6%; Score 464; DB 2; Length 133;
Best Local Similarity 68.8%; Pred. No. 9.4e-42;
Matches 88; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

QY 1 MNHTSQAFITTAASGGOPPNYERKEEYEAEMGAPHGASASVRTTVINMPREVSVPDHVW 60
Db 1 MSHTVQTFSPVNSGGOPPNYEMLEKEEBEHAVALGCPHPNPAPPTSTVIHIRSTVSPDHVW 60
QY 61 SLFNTLPMNFCCLGFTAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 61 SLFNTLPMNFCCLGFTAFAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNIWALILGILMTIL 120
QY 121 TIVSVIII 128
Db 121 LIVIPVLI 128
RESULT 3
S17183
interferon-induced protein 1-8D - human
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C:Accession: S17183
R:Lewin, A.R.; Reid, L.B.; McMahon, M.; Stark, G.R.; Kerr, I.M.
Eur. J. Biochem. 199, 417-423, 1991
A:Title: Molecular analysis of a human interferon-inducible gene family.
A:Reference number: S17182; MUID:91301153; PMID:1906403
A:Accession: S17183
A:Molecule type: DNA
A:Residues: 1-132 <LEW>
A:Cross-references: UNIPROT:Q01629; EMBL:X57351; NID:g311373; PIDN:CAA40625.1; PID:g22339
Query Match 64.4%; Score 449; DB 2; Length 132;
Best Local Similarity 65.4%; Pred. No. 3.6e-40;
Matches 87; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
QY 1 MNHTSQAFITTAASGGOPPNYERKEEYEAEMGAPHGASASVRTTVINMPREVSVPDHVW 60
Db 1 MNHIVQTF-SPVNSGGOPPNYEMLEKEEVAVLGCPHPNPAPPTSTVIHIRSTVSPDHVW 59
QY 61 SLFNTLPMNFCCLGFTAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 60 SLFNTLPMNFCCLGFTAFAYAYSVKSRDRKMWGDVTGAQAYASTAKCLNIWALILGIFMTIL 119
QY 121 TIVSVIIIVLNAQ 133
Db 120 LVI-IPVLVVQAQ 131
RESULT 4
A31454
interferon-inducible protein - human (clone 9-27)
C:Species: Homo sapiens (man)
C:Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004
C:Accession: A31454
R:Reid, L.E.; Brasnett, A.H.; Gilbert, C.S.; Porter, A.C.G.; Gewert, D.R.; Stark, G.R.;
Proc. Natl. Acad. Sci. U.S.A. 86, 840-844, 1989
A:Title: A single DNA response element can confer inducibility by both alpha- and gamma-
A:Reference number: A31454; MUID:89128873; PMID:2492664
A:Accession: A31454
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-125 <REI>
A:Cross-references: UNIPROT:P13164; GB:J04164; NID:g177801; PIDN:AAA35494.1; PID:g177802
Query Match 55.5%; Score 387; DB 2; Length 125;
Best Local Similarity 72.8%; Pred. No. 1.2e-33;
Matches 75; Conservative 13; Mismatches 15; Indels 0; Gaps 0;
QY 24 KEEYEAEMGAPHGASASVRTTVINMPREVSVPDHVWVSLFNTLPMNFCCLGFTAYAYSVK 83
Db 3 KEEBEAVALGAPPSTILPRSTVINIHSETSVDPDHVWVSLFNTLFLNWCCLGIFAFAYSVK 62
QY 84 SRDRKMWGDVTGAQAYASTAKCLNISTLVLSILMVITIVSVI 126
Db 63 SRDRKMWGDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105

RESULT 5
S00742
cytochrome-c oxidase (BC 1.9.3.1) chain I - Tetrahymena pyriformis mitochondrion
C:Species: mitochondrion Tetrahymena pyriformis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: S00742
R:Ziaie, Z.; Suyama, Y.
Curr. Genet. 12, 357-368, 1987
A:Title: The cytochrome oxidase subunit I gene of Tetrahymena: a 57 amino acid NH2-termi
A:Reference number: S00742; MUID:88184706; PMID:2833363
A:Accession: S00742
A:Molecule type: DNA
A:Residues: 1-698 <ZIA>
A:Cross-references: UNIPROT:P11947; EMBL:X06133
C:Genetics:
A:Genetic code: SGC6
A:Start codon: ATA
C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-ass
transmembrane protein
F:59-617/Domain: cytochrome-c oxidase chain I homology <COI>
F:111-538/Binding site: heme a iron (His) (axial ligands) #status predicted
F:401-450-451/Binding site: copper (His) #status predicted
F:401-405/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F:405/Binding site: oxygen (Tyr) #status predicted
F:528/Binding site: magnesium (His) (shared with chain II) #status predicted
F:536/Binding site: heme a3 iron (His) (axial ligand) #status predicted
Query Match 12.0%; Score 83.5; DB 1; Length 698;
Best Local Similarity 22.9%; Pred. No. 1;
Matches 27; Conservative 14; Mismatches 54; Indels 23; Gaps 3;
QY 3 HTSQAFITTAASGGQP-----PN-YERIKEEYEAEMGAPHGASASVRTTVINMP 49
Db 375 HWQTFEYAYGGDPILSQHLFWFFGHPEVYVLIPTFGFINNVDPH-----NNT 424
QY 50 REVSVDPDHVWVSLFNTLPMNFCCLGFTAYAYSVKGRDRKMWGDVTGAQAYASTAKCLN 107
Db 425 RRVASKHHMIWAIYVMAYMGLVWGHMVLGLDHRSTRMYSTITITIMSPATIKYVN 482
RESULT 6
AF1421
hypothetical membrane protein lmo2775 [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AF1421
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihl, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kieft, J.; Kuhn, M.; Kunat, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AF1421
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-722 <GLA>
A:Cross-references: UNIPROT:Q8Y3Q8; GB:NC_003210; PIDN:CAD00988.1; PID:g16412275; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo2775
Query Match 11.9%; Score 83; DB 2; Length 722;
Best Local Similarity 21.8%; Pred. No. 1.2;
Matches 24; Conservative 25; Mismatches 47; Indels 14; Gaps 3;
QY 20 YERIKEEYEAEMGAPHGASASVRTTVINMPREVSVPDHVWVSLFNTLPMNFCCLGFIAYA 79
Db 20 YERIKEEYEAEMGAPHGASASVRTTVINMPREVSVPDHVWVSLFNTLPMNFCCLGFIAYA 79

Db 157 YQAFLEKEP-----QYGEVTTKSDVSWWKYINIP-----LMTLLCFAILFVFTYY 204

Qy 80 YSVKSRDRKMWGDVTAQAYASTAKCLN--ISTLVLSILMVVITIVSVII 127

Db 205 YLRYSKQRLVNRINGNSLVTLMSLENKTIIFTLSVLAILITFVSIVL 254

RESULT 7

ODPPI

Cytochrome-c oxidase (EC 1.9.3.1) chain I - Paramacium sp. mitochondrion

N:Alternate names: cytochrome a3 polypeptide I; cytochrome a3 polypeptide I

C:Species: mitochondrion Paramacium sp.

C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004

C:Accession: A24988

R:Pritchard, A.E.; Seilhamer, J.J.; Cummings, D.J.

Gene 44, 243-253, 1986

A:Title: Paramacium mitochondrial DNA sequences and RNA transcripts for cytochrome oxidase

A:Reference number: A91555; MUID:87055241; PMID:3023187

A:Accession: A24988

A:Molecule type: DNA

A:Residues: 1-645 <PRI>

A:Cross-references: UNIPROT:P05489; GB:M15281; NID:G342944; PIDN:AAA79251.1; PID:g101962

A:Note: in GenBank entry ODPPI, release 109.0, PID:g1019626 assumes special genetic code

C:Genetics:

A:Gene: COI

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology

C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-associated protein

F:2-559/Domain: cytochrome-c oxidase chain I homology <COI>

F:54,480/Binding site: heme a iron (His) (axial ligands) #status predicted

F:343,392,393/Binding site: copper (His) #status predicted

F:343-347/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted

F:347/Binding site: oxygen (Tyr) #status predicted

F:470/Binding site: magnesium (His) (shared with chain II) #status predicted

F:478/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 11.5%; Score 80; DB 1; Length 645;

Best Local Similarity 24.0%; Pred. No. 2.2;

Matches 30; Conservative 24; Mismatches 65; Indels 6; Gaps 4;

Qy 3 HTSQAFITPAAGGQPPNRYRIKEY---EVAEMGAP-HGSASVRTTINMPREVSVDPHV 58

Db 317 HWQTSFDFAYGGDPILFQHLFWFGHPGVYILIPSGVANIVLPFVTM-RRMSSKHHM 375

Qy 59 VWSLFNTLFWNFCLGFTAYAYSVKSRDRKMWGDVTAQAYASTAKCLNISTLVLSILMV 118

Db 376 IWAVYVMAYMGFVWVGHMHYLVGLDHRSRNIYSTITIMICLPATIKLVN-WTLTLANAAI 434

Qy 119 VITIV 123

Db 435 HVDLV 439

RESULT 9

T09067

extensin-like protein NG5 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09067

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: 216543

A:Accession: T09067

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 <ROW>

A:Cross-references: UNIPROT:O35449; EMBL:AF030001; NID:g2564945; PID:g2564955

C:Genetics:

A:Gene: NG5

A:Map position: 17

A:Introns: 7/1; 186/3; 248/3

Query Match 11.0%; Score 76.5; DB 2; Length 306;

Best Local Similarity 21.5%; Pred. No. 2.3;

Matches 29; Conservative 25; Mismatches 64; Indels 17; Gaps 4;

Qy 15 GQPPNRYRIKEYEVAEMGAPH-----GSASVRTTINMPR-----EVSVPDHHVWSL 62

Db 167 GYPLQLQPCATAYVPVVGTPYAGTGGPCVSTLPPPGGGLALLEPRPPHDYMPI 226

Qy 63 FNTLFWNFCLL---GFTAYAYSVKSRDRKMWGDVTAQAYASTAKCLNISTLVLSILMV 119

Db 227 --AVLTITCCFPWPTGIIAIPKAVQRTALARGDLVSAEIASREARNFSFISLVGIAAMV 284

Qy 120 ITIVSVIIIVLNAQN 134

Db 285 LCTILTIVIIIAAQH 299

RESULT 10

T31092

probable voltage-gated sodium channel - Aiptasia pallida

C:Species: Aiptasia pallida

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

A:Genome: mitochondrion

A:Genetic code: SGC6

A:Start codon: ATA

C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology

C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane-associated protein

F:2-559/Domain: cytochrome-c oxidase chain I homology <COI>

F:54,480/Binding site: heme a iron (His) (axial ligands) #status predicted

F:343,392,393/Binding site: copper (His) #status predicted

F:343-347/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted

F:347/Binding site: oxygen (Tyr) #status predicted

F:470/Binding site: magnesium (His) (shared with chain II) #status predicted

F:478/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 11.5%; Score 80; DB 1; Length 645;

Best Local Similarity 24.0%; Pred. No. 2.2;

Matches 30; Conservative 24; Mismatches 65; Indels 6; Gaps 4;

Qy 3 HTSQAFITPAAGGQPPNRYRIKEY---EVAEMGAP-HGSASVRTTINMPREVSVDPHV 58

Db 317 HWQTSFDFAYGGDPILFQHLFWFGHPGVYILIPSGVANIVLPFVTM-RRMSSKHHM 375

Qy 59 VWSLFNTLFWNFCLGFTAYAYSVKSRDRKMWGDVTAQAYASTAKCLNISTLVLSILMV 118

Db 376 IWAVYVMAYMGFVWVGHMHYLVGLDHRSRNIYSTITIMICLPATIKLVN-WTLTLANAAI 434

Qy 119 VITIV 123

Db 435 HVDLV 439

RESULT 9

T09067

extensin-like protein NG5 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: T09067

R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S.

A:Description: Sequence of the mouse major histocompatibility locus class III region.

A:Reference number: 216543

A:Accession: T09067

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-306 <ROW>

A:Cross-references: UNIPROT:O35449; EMBL:AF030001; NID:g2564945; PID:g2564955

C:Genetics:

A:Gene: NG5

A:Map position: 17

A:Introns: 7/1; 186/3; 248/3

Query Match 11.0%; Score 76.5; DB 2; Length 306;

Best Local Similarity 21.5%; Pred. No. 2.3;

Matches 29; Conservative 25; Mismatches 64; Indels 17; Gaps 4;

Qy 15 GQPPNRYRIKEYEVAEMGAPH-----GSASVRTTINMPR-----EVSVPDHHVWSL 62

Db 167 GYPLQLQPCATAYVPVVGTPYAGTGGPCVSTLPPPGGGLALLEPRPPHDYMPI 226

Qy 63 FNTLFWNFCLL---GFTAYAYSVKSRDRKMWGDVTAQAYASTAKCLNISTLVLSILMV 119

Db 227 --AVLTITCCFPWPTGIIAIPKAVQRTALARGDLVSAEIASREARNFSFISLVGIAAMV 284

Qy 120 ITIVSVIIIVLNAQN 134

Db 285 LCTILTIVIIIAAQH 299

RESULT 10

T31092

probable voltage-gated sodium channel - Aiptasia pallida

C:Species: Aiptasia pallida

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004

C;Accession: T31092
R;White, G.B.; Pfahl, A.; Haddock, S.; Lamers, S.; Greenberg, R.M.; Anderson, P.A.V.
submitted to the EMBL Data Library, January 1998
A;Description: Structure of a putative sodium channel from the sea anemone *Aiptasia pallida*
A;Reference number: Z20975
A;Accession: T31092
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-1810 <WHI>
A;Cross-references: UNIPROT:O44930; EMBL:AF041851; NID:g2791840; PID:g2791841; PIDN:AA89
C;Genetics:
A;Gene: NaI
C;Superfamily: sodium channel protein

Query Match 10.8%; Score 75; DB 2; Length 1810;
Best Local Similarity 24.4%; Pred. No. 22;
Matches 33; Conservative 23; Mismatches 39; Indels 40; Gaps 8;

QX 19 NYERIKEEYEVAEMGA-----PHGSA---SVRTTIVNMPREV-SVPDH--VVM----- 60
DB 1309 NFRLKKQYB--DFGALDVLTTSQRAWFGTIRRAATKPKKVISRPENSMALFDVIH 1366
QY 61 -SLFNTLFMNFCLGFIAYAYSVKSRDRKMGVDVTGAQAYA---STAKCLINISTLVLSIL 116
DB 1367 SSRFETLMFFICLNIL-----VVMQHYGQKPAVEQALMIINLVFTGL 1410
QY 117 MVVITVSVIIIVLN 131
DB 1411 FTLEAILRIIVLRLH 1425

RESULT 11
A70839
N;Alternative names: membrane protein MLCL622 homolog
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: A70839
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Suleston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: A70839
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-412 <COL>
A;Cross-references: UNIPROT:O53655; GB:AL021928; GB:AL123456; NID:g3261522; PIDN:CAA1732
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: Rv0204c

Query Match 10.5%; Score 73.5; DB 2; Length 412;
Best Local Similarity 33.8%; Pred. No. 6.5;
Matches 23; Conservative 11; Mismatches 27; Indels 7; Gaps 3;

QY 60 WSLFNTLFMNFCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLINISTLVLSILMVV 119
DB 258 WSLFNMW-ADVACLGFAAYA---AGDHASVGGI--AVAYAAARAVGTIPLMPGGVLVVE 310
QY 120 ITIVSVII 127
DB 311 AVLVPGLV 318

RESULT 12
S75757
hypothetical protein sll046 - *Synechocystis* sp. (strain PCC 6803)
C;Species: *Synechocystis* sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S75757
R;Kaneke, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75757
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-84 <KAN>
A;Cross-references: UNIPROT:P74772; EMBL:D64003; GB:AB001339; NID:g1001200; PIDN:BA01049;
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 10.4%; Score 72.5; DB 2; Length 84;
Best Local Similarity 29.3%; Pred. No. 1.5;
Matches 24; Conservative 13; Mismatches 40; Indels 5; Gaps 2;

QY 54 VPDHVVMSLFNTLFMNFCC--LGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLINISTL 111
DB 6 VPNLAQSIIVTL---FCLPLGIVAIIRKASEVNSRLASGDYEGAVKASKEAKKFCWWSF 62
QY 112 VLSILMVVITIVSVIIIVLNAQ 133
DB 63 GAGIIFIAYFVLVIAAVFGQ 84

RESULT 13
S40702
hypothetical protein C07A9.10 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40702
R;Smith, M.
submitted to the EMBL Data Library, December 1993
A;Reference number: S40701
A;Accession: S40702
A;Molecule type: DNA
A;Residues: 1-254 <SMI>
A;Cross-references: UNIPROT:P34321; EMBL:Z29094; NID:g436440; PID:g436442
C;Genetics:
A;Introns: 61/3; 82/1; 184/3

Query Match 10.3%; Score 72; DB 2; Length 254;
Best Local Similarity 19.1%; Pred. No. 5.5;
Matches 35; Conservative 26; Mismatches 56; Indels 66; Gaps 7;

QY 1 MNHTSOAFITAAAG---GPPN--YERIKEEYEVAEMG---APHGS-----ASVR 42
DB 1 MHTTDRMVSHKKRPVGPMPRWTDLSRKEITTRDMGNIIITPWSQAKDRKAWKAVIR 60
QY 43 TTVINMPREVSVDPDHV-----VMSLFNTLFMNF- 70
DB 61 TTETREPKNIIKQVTLVFOANATISGPPVLPRPVKIHASSYLSRLNLGDDCFMNV 120
QY 71 -----CCLGFI-AYAYSVKSRDRKMGVDVTGAQAYASTAKCLINISTLVLS 114
DB 121 LQLLKSSPEDHFRITCCVGTIHEELKILSGEKVDVGLRRMHYSKLHKGKRNCTALK 180
QY 115 ILM 117
DB 181 VLM 183

RESULT 14
H97249
protein containing aminopeptidase domain (iap family) [imported] - *Clostridium acetobutylicum*
C;Species: *Clostridium acetobutylicum*
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: H97249
R;Nolling, J.; Berton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

Search completed: June 18, 2005, 16:35:29
Job time : 40 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:28:00 ; Search time 43 Seconds
(without alignments)
237.835 Million cell updates/sec

Title: US-10-621-911A-2
Perfect score: 697
Sequence: 1 MNHTSQAFITAAAGGPPNY.....VITIVSVIIIVLNAQLHT 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_AA*
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3: /cgm2_6/ptodata/1/iaa/6A_COMB.pap:*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pap:*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pap:*
6: /cgm2_6/ptodata/1/iaa/backfiles.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473	67.9	133	4	US-09-370-838-124
2	473	67.9	133	4	US-09-854-133-124
3	464	66.6	133	4	US-09-461-912A-37
4	381	54.7	125	5	PCT-US93-06829-2
5	376	53.9	125	5	PCT-US93-06829-17
6	370	53.1	125	5	PCT-US93-06829-13
7	370	53.1	125	5	PCT-US93-06829-15
8	366	52.5	125	5	PCT-US93-06829-16
9	365	52.4	125	5	PCT-US93-06829-14
10	364	52.2	125	5	PCT-US93-06829-12
11	72	10.3	690	3	US-08-935-433-2
12	72	10.3	690	3	US-09-553-132-2
13	72	10.3	706	4	US-09-949-016-11394
14	71.5	10.3	318	2	US-09-027-013-4
15	71.5	10.3	318	3	US-09-244-233-4
16	69.5	10.0	746	4	US-09-589-892B-2
17	68	9.8	219	2	US-08-855-140-4
18	68	9.8	448	4	US-09-323-195A-18
19	67.5	9.7	256	4	US-09-270-767-46799
20	66.5	9.5	404	4	US-09-252-991A-23011
21	66	9.5	240	3	US-09-134-001C-4180
22	66	9.5	270	1	US-08-347-471-4
23	66	9.5	310	4	US-09-509-738C-24
24	65.5	9.4	444	4	US-09-540-236-1993
25	65.5	9.4	539	4	US-09-538-082-741
26	65	9.3	299	4	US-09-520-781-28
27	65	9.3	391	4	US-09-721-870-34

28	65	9.3	1051	3	US-09-134-001C-5005	Sequence 5005, Ap
29	64.5	9.3	689	3	US-09-499-964-1	Sequence 1, Appli
30	64.5	9.3	1116	4	US-09-543-681A-4379	Sequence 4379, Ap
31	64	9.2	255	4	US-09-248-796A-20672	Sequence 20672, A
32	64	9.2	1621	1	US-08-242-677-2	Sequence 2, Appli
33	63.5	9.1	303	4	US-09-328-352-7717	Sequence 7717, Ap
34	63.5	9.1	810	4	US-09-902-540-12414	Sequence 12414, A
35	63.5	9.1	1191	4	US-09-248-796A-16243	Sequence 16243, A
36	63	9.0	163	4	US-09-438-185A-244	Sequence 244, App
37	63	9.0	168	3	US-09-087-465-32	Sequence 32, Appl
38	63	9.0	287	4	US-09-248-796A-20822	Sequence 20822, A
39	63	9.0	605	3	US-09-394-645-2	Sequence 2, Appli
40	63	9.0	605	3	US-09-243-560B-2	Sequence 2, Appli
41	63	9.0	737	3	US-09-511-625B-2	Sequence 2, Appli
42	63	9.0	819	3	US-09-511-625B-2	Sequence 4, Appli
43	63	9.0	847	1	US-08-276-099A-2	Sequence 2, Appli
44	63	9.0	847	1	US-08-781-850-2	Sequence 2, Appli
45	63	9.0	847	3	US-09-087-465-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-370-838-124
; Sequence 124, Application US/09370838
; Patent No. 6444425
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raodoh
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
; TITLE OF INVENTION: LUNG CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.475C1
; CURRENT APPLICATION NUMBER: US/09/370,838
; CURRENT FILING DATE: 1999-08-09
; EARLIER APPLICATION NUMBER: US 09/285,323
; EARLIER FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 289
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 124
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-370-838-124

Query Match	67.9%	Score 473;	DB 4;	Length 133;
Best Local Similarity	70.3%;	Pred. No. 6.9e-52;		
Matches	90;	Conservative 14;	Mismatches 24;	Indels 0; Gaps 0;
Qy	1	MNHTSQAFITAAAGGPPNYERIKKEEYEAEMGAPHGASV	RTTVINNPREVSPDHVVW	60
Db	1	MNHTVQTFPPVNSGQPPNYEMLKEHEVAVLGAPHPAPPT	STVIHIRSTVPDHVVW	60
Qy	61	SLFNTLPMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYAS	TAKCLNISTIVLSILMVVI	120
Db	61	SLFNTLPMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYAS	TAKCLNISTIVLSILMVVI	120
Qy	121	TVIVPVLI 128		
Db	121	LIVIPVLI 128		
RESULT 2				
US-09-854-133-124				
; Sequence 124, Application US/09854133				
; Patent No. 6759508				
; GENERAL INFORMATION:				
; APPLICANT: Lodes, Michael J.				
; APPLICANT: Mohamath, Raodoh				
; APPLICANT: Henderson, Robert A.				
; APPLICANT: Benson, Darin R.				

APPLICANT: Secretist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 124
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapien
US-09-854-133-124

Query Match 67.9%; Score 473; DB 4; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-52;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MNHTSOAFITAAGGQPPNYERKEEYEAEMGAPHGASVTRTVINMPREVSVPDHVW 60
Db 1 MNHTVQTFPSVNSGQPPNYEMLEKEHEVAVLGPHNPAPTSTVIHIRSTSVDPHVW 60

Qy 61 SLFNTLPMNCCGLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWVI 120
Db 61 SLFNTLPMNCCGLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWVI 120

Qy 121 TIVSVIII 128
Db 121 LIVIPVLI 128

RESULT 3
US-09-461-912A-37
Sequence 37, Application US/09461912A
Patent No. 6709855
GENERAL INFORMATION:
APPLICANT: Stanton, Lawrence A.
APPLICANT: White, R. Tyler
APPLICANT: Damm, Deborah L.
APPLICANT: Lewicki, John A.
TITLE OF INVENTION: Methods for detection and use of
FILE REFERENCE: SCIOS.011A
CURRENT APPLICATION NUMBER: US/09/461,912A
CURRENT FILING DATE: 1999-12-15
PRIOR FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 48
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 133
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (238).... (639)
US-09-461-912A-37

Query Match 66.6%; Score 464; DB 4; Length 133;
Best Local Similarity 68.8%; Pred. No. 9.6e-51;
Matches 88; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MNHTSOAFITAAGGQPPNYERKEEYEAEMGAPHGASVTRTVINMPREVSVPDHVW 60
Db 1 MSHTVQTFPSVNSGQPPNYEMLEKEHEVAVLGPHNPAPTSTVIHIRSTSVDPHVW 60

Qy 61 SLFNTLPMNCCGLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWVI 120
Db 61 SLFNTLPMNCCGLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWVI 120

Qy 121 TIVSVIII 128
Db 121 LIVIPVLI 128

RESULT 4
PCT-US93-06829-2
Sequence 2, Application PC/TUS9306829
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Constantoulakis, Pantelis
APPLICANT: Felber, Barbara K.
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart St. Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-06829-2

Query Match 54.7%; Score 381; DB 5; Length 125;
Best Local Similarity 71.8%; Pred. No. 2.8e-40;
Matches 74; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 24 KEEYEVAEMGAPHGASVTRTVINMPREVSVPDHVWVSLFNTLPMNCCGLGFIAYAYSVK 83
Db 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVDPHVWVSLFNTLFLNMCCGLGFIAYAYSVK 62

Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWVITIVSVI 126
Db 63 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMWITIGFILSV 105

RESULT 5
PCT-US93-06829-17
Sequence 17, Application PC/TUS9306829
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Constantoulakis, Pantelis
APPLICANT: Felber, Barbara K.
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart St. Tower

CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-06829-17

Query Match 53.9%; Score 376; DB 5; Length 125;
Best Local Similarity 62.4%; Pred. No. 1.2e-39;
Matches 73; Conservative 17; Mismatches 17; Indels 10; Gaps 1;

QY 24 KEEVEVAEMGAPHGASVRTTVINMPREVSPDHVWSLNTLFMNFCLGFIAYAVSVK 83
DB 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHGWSLNTLFNWCCLGFIAPAVSVK 62
QY 84 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMV-----ITIVSVIIVL 130
DB 63 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMV-----ITIVSVIIVL 119

RESULT 6
PCT-US93-06829-13
Sequence 13, Application PC/TUS9306829
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Constantoulakis, Pantelis
APPLICANT: Felber, Barbara K.
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart St. Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213

FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-06829-13

Query Match 53.1%; Score 370; DB 5; Length 125;
Best Local Similarity 69.9%; Pred. No. 7e-39;
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 24 KEEVEVAEMGAPHGASVRTTVINMPREVSPDHVWSLNTLFMNFCLGFIAYAVSVK 83
DB 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHGWSLNTLFNWCCLGFIAPAVSVK 62
QY 84 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMVITIVSVI 126
DB 63 SRDRKMGVDVTGAQAYASTAKCLNISTVLISILMVITIVSVI 105

RESULT 7
PCT-US93-06829-15
Sequence 15, Application PC/TUS9306829
GENERAL INFORMATION:
APPLICANT: Pavlakis, George N.
APPLICANT: Constantoulakis, Pantelis
APPLICANT: Felber, Barbara K.
TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart St. Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

PCT-US93-06829-15

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Query Match      53.1%; Score 370; DB 5; Length 125;
Best Local Similarity 69.9%; Pred.No. 7e-39;
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

QY 24 KEYEYVAMGAPGHGSASVRTVITNMPREVSVDPDHVVMVMSLFTNTLPMNFCCLGTAIAYSVK 83
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 3  KESHEAVLGAFTPTTLPRSGAINIHSETVDPDHVVMVMSLFTNTLFLNCCCLGTAIAYSVK 62
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 84 SRDRKMWGDVTGAQAAVASTAKCLNISTLVLSIMVVTIVSVI 126
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
DB 63 SRDRKMWGDVTGAQAAVASTAKCLNIAWILGILMTIGFILSLV 105
      |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESIN.T A

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PCT-US93-06829-16
; Sequence 16, Application PC/TUS9306029
; GENERAL INFORMATION:
;
; APPLICANT: Pavlakis, George N.
; APPLICANT: Constantoulakis, Pantelis
; APPLICANT: Feiber, Barbara K.
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
; - TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
; NUMBER OF SEQUENCES: 17
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105-1492

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-06829-16

[illegible]

63 SGARKWVGDVTGAQAYASTAKCLNIWALILGILMTIGFILSLV 105

RESULT 9

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PCT-US93-06829-14
; Sequence 14, Application PC/TUS9306829
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Constantoulakis, Pantelis
; APPLICANT: Felber, Barbara K.
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
; TITLE OF INVENTION: INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
;

```

COUNTRY: USA
ZIP: 94105-1

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/06829
FILING DATE: 19930720
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/917,213
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 15280-67
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-06829-14

```

Query Match	52.4%	Score 365;	DB 5;	Length 125;
Best Local Similarity	69.9%;	Pred. No. 36-38;		
Matches 72: Conservative	13: Mismatches	18: Indels	0: Gaps	0:

Qy	24	KEBEYVAEMGAPHGASVTRTVINMPREVSVDPDHVWLSFNTLFLMNFCCLGFIAYAYSVK	83
Db	3	KEBEHAVILGAPPSTILPRSTVINIHSETSVDPDHVWMSGANTLFLNWCCLGFIAYAYSVK	62
Qy	84	SDRDKMWGVDVTCQAQAYASTAKCLNISTLVLILMVVITVSVI	126
Db	63	SDRDKMWGVDVTCQAQAYASTAKCLNITWALILGILITIGILSLV	105

RESULT 10

```

PCT-US93-06829-12
; Sequence 12, Application PC/TUS9306829
; GENERAL INFORMATION:
; APPLICANT: Pavlakis, George N.
; APPLICANT: Constantoulakis, Pantelis
; APPLICANT: Felber, Barbara K.
; TITLE OF INVENTION: INHIBITION OF RETROVIRAL EXPRESSION BY
; INTERFERON-INDUCED CELLULAR GENES AND PROTEINS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Steuart St. Tower
; CITY: San Francisco
; STATE: CA
;

```

```

; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06829
; FILING DATE: 19930720
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/917,213
; FILING DATE: 07-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 15280-67
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; PCT-US93-06829-12

Query Match 52.2%; Score 364; DB 5; Length 125;
Best Local Similarity 69.9%; Pred. No. 4e-38;
Matches 72; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 24 KEEVEAEMGPHGASVTRTVINPREVSDPDHVVWSLNTLFNMFCLGFIAYAVSVK 83
Db 3 KEEHEVAIVAGPSTILPRSTVINIHSETSVPGAVVWSLNTLFNMFCLGFIAYAVSVK 62

Qy 84 SRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVITVSVI 126
Db 63 SRDRKMGVDVTGAQAYASTAKCLNIWALLILGILMTIGFILSIV 105

RESULT 11
US-08-935-433-2
; Sequence 2, Application US/08935433
; Patent No. 6319688
; GENERAL INFORMATION:
; APPLICANT: FEILD, JOHN
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE
; TITLE OF INVENTION: TRANSPORTER (IPT-1)
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,433
; FILING DATE: 23-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/044,974
; FILING DATE: 28-APR-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F

; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 690 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-935-433-2

Query Match 10.3%; Score 72; DB 3; Length 690;
Best Local Similarity 20.6%; Pred. No. 4.3;
Matches 33; Conservative 34; Mismatches 61; Indels 32; Gaps 6;

Qy 8 PITAAGGQPPNYERIKEEYEVAEMGPHGASV-----RTVINMPREVSV----- 55
Db 17 YLEGAAGQQPTAPDKSKETNKTNDTEAPVTKIELLPSYSTATLIDETEVDDPNNLPTLQ 76

Qy 56 -DHVVWSLNTLFNMF-----CLGFIAY-----AYSVKSRDRKMGVDVTGAQAYAS 101
Db 77 DSGIKWSEDTGKILCFQIGIRLILLGLFYFVCSLDILSSAFQLVGGKMACQFFSN 136

Qy 102 TAKCLN-ISTLVLSILMWI-----TIVSVIIIVLNAQNL 135
Db 137 SSIMSNPLGLVIGVLTVLVQSSSTSTSIIVVSMVSSSLL 176

RESULT 12
US-09-553-132-2
; Sequence 2, Application US/09553132
; Patent No. 6350858
; GENERAL INFORMATION:
; APPLICANT: FEILD, JOHN
; TITLE OF INVENTION: A HUMAN SODIUM DEPENDENT PHOSPHATE
; TITLE OF INVENTION: TRANSPORTER (IPT-1)
; FILE REFERENCE: -GH-70006-D1
; CURRENT APPLICATION NUMBER: US/09/553,132
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/044,974
; PRIOR FILING DATE: 1997-04-28
; PRIOR APPLICATION NUMBER: 08/935,433
; PRIOR FILING DATE: 1997-09-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-553-132-2

Query Match 10.3%; Score 72; DB 3; Length 690;
Best Local Similarity 20.6%; Pred. No. 4.3;
Matches 33; Conservative 34; Mismatches 61; Indels 32; Gaps 6;

Qy 8 PITAAGGQPPNYERIKEEYEVAEMGPHGASV-----RTVINMPREVSV----- 55
Db 17 YLEGAAGQQPTAPDKSKETNKTNDTEAPVTKIELLPSYSTATLIDETEVDDPNNLPTLQ 76

Qy 56 -DHVVWSLNTLFNMF-----CLGFIAY-----AYSVKSRDRKMGVDVTGAQAYAS 101
Db 77 DSGIKWSEDTGKILCFQIGIRLILLGLFYFVCSLDILSSAFQLVGGKMACQFFSN 136

Qy 102 TAKCLN-ISTLVLSILMWI-----TIVSVIIIVLNAQNL 135
Db 137 SSIMSNPLGLVIGVLTVLVQSSSTSTSIIVVSMVSSSLL 176

RESULT 13
```

```
US-09-949-016-11394
; Sequence 11394, Application US/09949016
; Patent No. 5812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11394
; LENGTH: 706
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11394

Query Match 10.3%; Score 72; DB 4; Length 706;
Best Local Similarity 20.6%; Pred. No. 4.4; Indels 32; Gaps 6;
Matches 33; Conservative 34; Mismatches 61;

QY 8 FITAAGCGQPPNYRIKEEYEAEMGAPHSASV-----RTTVINMPREVSV----- 55
DB 33 YLEGAAGQQTAPDKSKETKNTDTEAPVTKIELLPSTATLIDETVEDDPWNLPTLQ 92
QY 56 -DHVWSLFTLFWNFC-----CLGFIAY--AYSVKSRDRKMGVDVTGAQAYAS 101
DB 93 DSGIKMSERDTGKILCFQIGRILLLGLFYFFVCSLDLSSAFOLVGGKMGAGOFFSN 152
QY 102 TAKCLN-ISTVLISLMVVI-----TIVSVIIIVLNAQNL 135
DB 153 SSIMSNNLLGLVGLVTVLVVQSSTSTSVMSVSSLL 192

RESULT 14
US-09-027-013-4
; Sequence 4, Application US/09027013
; Patent No. 5962302
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN N-ACETYLNEURAMINATE LYASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,013
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
```

```
; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
US-09-027-013-4

Query Match 10.3%; Score 71.5; DB 2; Length 318;
Best Local Similarity 19.0%; Pred. No. 1.7;
Matches 19; Conservative 21; Mismatches 29; Indels 31; Gaps 3;

QY 21 ERIKEEYEAEMGAPHSASVRTTVINMPREVSVDPHVWSLFTLFWNFCCLGPF---IA 77
DB 199 ERVKRAY-----PDHLIWAGFDEMMLPACSLGIDGAG 231
QY 78 YAVSVKSRDRKMGVDVTGAQAYASTAKCLNIST-LVLSIL 116
DB 232 STFNNAKARQIFELSKAGKYDEALEVQHVTVNDLIAGIL 271

RESULT 15
US-09-244-233-4
; Sequence 4, Application US/09244233
; Patent No. 6030824
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN N-ACETYLNEURAMINATE LYASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/244,233
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/027,013
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0462 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: GI 1016806
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US-09-244-233-4

Query Match 10.3%; Score 71.5; DB 3; Length 318;
Best Local Similarity 19.0%; Pred. No. 1.7;
Matches 19; Conservative 21; Mismatches 29; Indels 31; Gaps 3;
QY 21 ERIKEEYVAEMGAPHGASVTTTINNPREVSVDHVVWSLFTLFWNFCCCLGF---IA 77
DB 199 ERVKRAY-----PDHLIWAGFDEMMLPACSLGIDGAIG 231
QY 78 VAYSVKSRDRKMWGVDVTGAQAYASTAKCLNIST-LVLSIL 116
DB 232 STFNVNKRARQIFELSKAGKYDEALEVQHVTNDLIAGIL 271

Search completed: June 18, 2005, 16:36:17
Job time : 44 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:12:19 ; Search time 161 Seconds
(without alignments)
329.107 Million cell updates/sec

Title: US-10-621-911A-2
Perfect score: 697
Sequence: 1 MNHTSQAFITRAGGQPPNY.....VVITIVSVIIIVLNAQNLT 137

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	697	100.0	137	5	ABG30945 Mouse GCR
2	697	100.0	137	8	ADJ76155 Marker ge
3	697	100.0	173	8	ABO84418 Mouse can
4	646	92.7	137	7	AD663837 Rat Prote
5	646	92.7	137	7	AD664615 Rat Prote
6	497	71.3	144	8	AD126260 Mouse Fra
7	473	67.9	133	2	AAY29544 Human lun
8	473	67.9	133	3	AB444556 Human lun
9	473	67.9	133	4	ABE13797 Human lun
10	473	67.9	133	6	ABR41053 Human MAP
11	473	67.9	133	7	ADD66432 Human lun
12	473	67.9	133	7	AD663839 Human Pro
13	473	67.9	133	7	ADD46417 Human Pro
14	473	67.9	133	7	AD667686 Human lun
15	473	67.9	143	5	ABP43105 Human ova
16	465	66.7	133	6	ABR41051 Human MAP
17	464	66.6	133	3	AAY93394 Protein e
18	464	66.6	133	6	ABR41052 Human MAP
19	461	66.1	143	4	ABG11590 Novel hum
20	454	65.1	132	6	ABR41089 Human MAP
21	454	65.1	132	6	ABO25123 Human 1-8
22	454	65.1	168	4	AB23517 Novel hum
23	453	65.0	132	6	ABR41088 Human MAP
24	453	65.0	132	8	AD107644 Human 1-8
25	453	65.0	156	7	ADE09084 Novel pro

26	452	64.8	146	7	ADE81103	Ad81103 Bovine 1-
27	452	64.8	146	8	ADI34857	Adi34857 Bovine pr
28	450	64.6	132	5	ABP64706	Abp64706 Human pro
29	450	64.6	132	8	AD126256	Ad126256 Human Fra
30	450	64.6	132	8	AD107646	Ad107646 Human 1-8
31	450	64.6	132	8	ABO84419	ABO84419 Human can
32	449	64.4	132	6	ABR92090	ABr92090 Human cer
33	449	64.4	132	6	ABR41050	ABr41050 Human MAP
34	449	64.4	132	8	ADQ29673	Adq29673 Human col
35	449	64.4	132	8	ABM81208	ABm81208 Tumour-as
36	449	64.4	132	8	ADP23176	Adp23176 PRO polyp
37	448	64.3	145	4	AM40509	Aam40509 Human pol
38	447	64.1	132	4	AAW38723	Aaw38723 Human pol
39	442	63.4	124	4	ABG11589	ABg11589 Novel hum
40	429.5	61.6	132	7	ADE95522	Ad95522 Human NOV
41	429.5	61.6	132	7	ADE95524	Ad95524 Human NOV
42	426.5	61.2	131	5	ABP42194	ABp42194 Human ova
43	412.5	59.2	155	8	ADP83527	Adp83527 Breast sp
44	388.5	55.7	107	8	AD126262	Ad126262 Mouse Fra
45	387	55.5	125	4	ABB50284	Abb50284 IFN-induc

ALIGNMENTS

RESULT 1
ABG30945
ID ABG30945 standard; protein; 137 AA.
XX
AC ABG30945;
XX
DT 21-OCT-2002 (first entry)
XX
DE Mouse GCR1/Fragilis protein.
XX
KW Mouse; GCR1; Fragilis; GCR2; Stella; pluripotent cell; PGC; transgenic;
KW primordial germ cell; germ tissue development; embryonic stem cell;
KW embryonic germ cell.
XX
OS Mus sp.
XX
FH Key
FT Region
FT Location/Qualifiers
FT 12..28
FT /note= "Anti-peptide antibody designed against this
FT 85..100
FT /note= "Anti-peptide antibody designed against this
FT sequence"

WO200257307-A2.
25-JUL-2002.
18-JAN-2002; 2002WO-GB0000215.
18-JAN-2001; 2001GB-00001300.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
Saitou M, Surani A;
WPI; 2002-590719/63.
N-PSDB; ABK90152.
GCR1 (Fragilis) and GCR2 (Stella) genes, useful for identifying and/or
isolating a pluripotent cell e.g., primordial germ cell.
Claim 13; Fig 1; 85pp; English.
The present invention relates to a new GCR1 (Fragilis) or GCR2 (Stella)
polypeptide, or its fragment, homologue, variant or derivative. The
homologue of, or antibody specific for, GCR1 or GCR2 is useful for
identifying and/or isolating a pluripotent cell, particularly PGC

CC (primordial germ cell) for studying germ tissue development and
 CC generation of transgenic animals, as well as embryonic stem cells or
 CC embryonic germ cells. The present amino acid sequence represents the
 CC mouse GCR1/Fragilis protein of the invention
 XX
 SQ Sequence 137 AA;
 Query Match 100.0%; Score 697; DB 5; Length 137;
 Best Local Similarity 100.0%; Pred. No. 5.1e-79;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNHTSQAFITAAAGGPPNRYERIKEEYEVAEMGAPHGASVRTTINMPREVSVPDHWVW 60
 DB 1 MNHTSQAFITAAAGGPPNRYERIKEEYEVAEMGAPHGASVRTTINMPREVSVPDHWVW 60
 QY 61 SLFNTLFMNFCCGFTIAYAYSVKSRDRKMVGDTGQAQYASTAKCLNISTLVLSILMVVI 120
 DB 61 SLFNTLFMNFCCGFTIAYAYSVKSRDRKMVGDTGQAQYASTAKCLNISTLVLSILMVVI 120
 QY 121 TIVSVIIIVLNAQLHT 137
 DB 121 TIVSVIIIVLNAQLHT 137
 RESULT 2
 ADU76155
 ID ADU76155 standard; protein; 137 AA.
 XX
 AC ADU76155;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Marker gene related amino acid sequence SEQ ID NO:1407.
 XX
 KW bronchial asthma; chronic obstructive pulmonary disease;
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
 KW gene therapy; marker.
 XX
 OS Mus musculus.
 XX
 PN EP1394274-A2.
 XX
 PD 03-MAR-2004.
 XX
 TF 04-AUG-2003; 2003EP-00254857.
 XX
 PR 06-AUG-2002; 2002JP-00229312.
 PR 20-MAR-2003; 2003JP-00077212.
 XX
 PA (GENO-) GENOX RES INC.
 XX
 PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
 XX
 DR WPI; 2004-193155/19.
 XX
 PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
 PT comparing the expression level of a marker gene in a biological sample
 PT from a subject with the expression level of the gene in a sample from a
 PT healthy subject.
 XX
 PS Claim 16; SEQ ID NO 1407; 241pp; English.
 XX
 CC The present invention describes a method of testing for bronchial asthma
 CC or chronic obstructive pulmonary disease. The method comprises
 CC determining the expression level of a marker gene in a biological sample
 CC from a subject, comparing the expression level determined with the
 CC expression level of the marker gene in a biological sample from a healthy
 CC subject, and judging whether the subject has bronchial asthma or chronic
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of
 CC genes (S1) whose expression levels increase when respiratory epithelial
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)
 CC whose expression levels decrease when respiratory epithelial cells are
 CC stimulated with interleukin-13. Also described: (1) a reagent (I) for

CC testing for bronchial asthma or chronic obstructive pulmonary disease;
 CC (2) a kit for screening for a candidate compound for a therapeutic agent
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
 CC an animal model for bronchial asthma or chronic obstructive pulmonary
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
 CC method for producing an animal model for bronchial asthma or chronic
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,
 CC a marker gene or an antisense nucleic acid corresponding to a portion of
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the
 CC expression of the gene through an RNAi effect or an antibody recognising
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a
 CC probe has been immobilised to assay a marker gene. (I) has respiratory
 CC and antiasthmatic activities, and can be used in gene therapy. The method
 CC is useful for testing for or screening for a therapeutic agent for
 CC bronchial asthma or chronic obstructive pulmonary disease. The present
 CC sequence is used in the exemplification of the present invention.
 XX
 SQ Sequence 137 AA;
 Query Match 100.0%; Score 697; DB 8; Length 137;
 Best Local Similarity 100.0%; Pred. No. 5.1e-79;
 Matches 137; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MNHTSQAFITAAAGGPPNRYERIKEEYEVAEMGAPHGASVRTTINMPREVSVPDHWVW 60
 DB 1 MNHTSQAFITAAAGGPPNRYERIKEEYEVAEMGAPHGASVRTTINMPREVSVPDHWVW 60
 QY 61 SLFNTLFMNFCCGFTIAYAYSVKSRDRKMVGDTGQAQYASTAKCLNISTLVLSILMVVI 120
 DB 61 SLFNTLFMNFCCGFTIAYAYSVKSRDRKMVGDTGQAQYASTAKCLNISTLVLSILMVVI 120
 QY 121 TIVSVIIIVLNAQLHT 137
 DB 121 TIVSVIIIVLNAQLHT 137
 RESULT 3
 ABO84418
 ID ABO84418 standard; protein; 173 AA.
 XX
 AC ABO84418;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Mouse cancer-associated protein MP14-034.1.
 XX
 KW Mouse; cancer-associated protein; cytostatic; cancer; leukaemia;
 KW lymphoma; CAP.
 XX
 OS Mus musculus.
 XX
 PN WO2004074320-A2.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-US0004730.
 XX
 PR 14-FEB-2003; 2003US-00367094.
 PR 14-MAR-2003; 2003US-0038838.
 PR 15-APR-2003; 2003US-00417375.
 PR 13-JUN-2003; 2003US-00461862.
 PR 15-SEP-2003; 2003US-00663431.
 PR 15-DEC-2003; 2003US-00737318.
 XX
 PA (SAGR-) SAGRES DISCOVERY INC.
 XX
 PI Morris DW, Morris DW, Malandro MS;
 XX
 DR WPI; 2004-652914/63.
 DR N-PSDB; ABO32561.
 XX

XX AC ADD46415;
XX DT 29-JAN-2004 (first entry)
XX DE Rat Protein CAA43655, SEQ ID NO 12095.
XX KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX OS chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX PN Rattus norvegicus.
XX PD W02003016475-A2.
XX PF 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEO) GEN HOSPITAL CORP.
XX PA (FARB) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; CAA43655.
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PT preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 101pp; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
XX CC which is differentially regulated in an animal subjected to pain and a
XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
XX CC modulates its activity is useful for preparing a medicament for treating
XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 137 AA;
Query Match 92.7%; Score 646; DB 7; Length 137;
Best Local Similarity 89.8%; Pred. No. 1.3e-72;
Matches 123; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 MNHTSQAFITAAAGQPPNYRIKEEYEAEMGAPHGASVRRITVNNPREVSPDHVW 60
DB 1 MNHTSQAFVNAATGGQPPNYRIKEEYEVSELGAPHGASVRRITVNNPREVSPDHVW 60

QY 61 SLFNTLPMNFCCLGFIAYAYSVKSRDKWVGDMTGAQAYASTAKCLNLSILMWVI 120
DB 61 SLFNTLPMNFCCLGFIAYAYSVKSRDKWVGDMTGAQAYASTAKCLNLSILMWVI 120
QY 121 TIVSVIIIVLNAQNLT 137
DB 121 TIVTVIIIALNAPRLQT 137
RESULT 6
ADI26260
ID ADI26260 standard; protein; 144 AA.
AC ADI26260;
DT 22-APR-2004 (first entry)
XX Mouse Fragilis 2 amino acid sequence SEQ ID NO:10.
DE Mouse Fragilis 2 amino acid sequence SEQ ID NO:10.
XX Fragilis; pluripotent cell; cytostatic; gene therapy; tumour;
KW choriocarcinoma; carcinoma; leiomyosarcoma; mouse.
XX Mus musculus.
PN W02004007723-A2.
XX 22-JAN-2004.
XX 17-JUL-2003; 2003WO-GB003093.
PR 17-JUL-2002; 2002GB-00016727.
PR 19-JUL-2002; 2002US-0397310P.
XX (UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.
XX Saitou M, Surani A;
WPI; 2004-122953/12.
N-PSDB; ADI26259.
XX New polypeptide comprising a human Stella or Fragilis amino acid
PT sequence, useful for treating or preventing testis, colon, stomach, germ
PT cell, choriocarcinoma, lung, large cell carcinoma, uterus, and
PT leiomyosarcoma.
XX Claim 3; SEQ ID NO 10; 189pp; English.
XX The present invention describes a polypeptide (I) comprising a human
CC Stella (SEQ ID No. 4, ADI26254) or Fragilis (SEQ ID No. 6, ADI26256)
CC amino acid sequence, its fragment, homologue, variant or derivative. Also
CC described: (1) a nucleic acid encoding (I), or its complement; (2) a
CC vector comprising the nucleic acid sequence; (3) a host cell comprising
CC the nucleic acid sequence; (4) a method for producing (I); (5) a method
CC for identifying a pluripotent cell; (6) an antibody capable of binding
CC specifically to (I); (7) a pluripotent cell identified by the method; (8)
CC a method of treatment or prophylaxis of a disease in an individual; (9) a
CC method of diagnosis or a disease; (10) a method of identifying a molecule
CC capable of binding to Stella or Fragilis; (11) a method of identifying a
CC modulator, preferably an agonist or antagonist of Stella or Fragilis;
CC (12) a modulator of Stella or Fragilis; (13) a transgenic non-human
CC animal; (14) a cell or tissue from the transgenic non-human animal; and
CC (15) a nucleic acid construct for functionally disrupting a Stella and/or
CC Fragilis gene in a host cell. (I) has cytostatic activity, and can be
CC used in gene therapy. The polypeptide (I), nucleic acids and methods are
CC useful for treating or preventing testis tumour, colon tumour, stomach,
CC germ cell tumours, choriocarcinoma, lung, large cell carcinoma, uterus,
CC and leiomyosarcoma. The antibody is useful for the identification and/or
CC isolation of a pluripotent cell. The transgenic non-human animal is
CC useful for identifying a compound, which is capable of interacting
CC specifically with a Stella or Fragilis protein. The present sequence
CC represents a mouse Fragilis 2 amino acid sequence, which is used in the
CC exemplification of the present invention.
XX


```
Db      61 SLFNTLFMNPCCGLGFIAPFAISVKSRRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Qy      121 TIVSVIII 128
Db      121 LIVIPVLI 128

RESULT 9
AAE13797
ID AAE13797 standard; protein; 133 AA.
XX
AC AAE13797;
XX
DT 26-FEB-2002 (first entry)
XX
DE Human lung tumour-specific protein SALT-T8.
XX
KW Human; lung tumour protein; immunostimulant; cytostatic; gene therapy;
KW antitense-therapy; vaccine; immune response; lung cancer; SALT-T8.
XX
OS Homo sapiens.
XX
PN WO200172295-A2.
XX
PD 04-OCT-2001.
XX
PF 28-MAR-2001; 2001WO-US0009991.
XX
PR 29-MAR-2000; 2000US-00538037.
XX
PR 05-JUN-2000; 2000US-00588937.
XX
PR 18-AUG-2000; 2000US-00640878.
XX
PR 22-SEP-2000; 2000US-0234517P.
XX
PR 01-NOV-2000; 2000US-00704512.
XX
PR 14-DEC-2000; 2000US-00738973.
XX
PA (CORI-) CORIXA CORP.
XX
PI Reed SG, Lodes MJ, Mohamath R, Secrist H, Benson DR, Indirias CV;
PI Henderson RA, Fling SP, Algate PA, Elliot M, Mannion J, Kalos WD;
XX
DR WPI; 2001-639201/73.
XX
DR N-PSDB; AAD23193.
XX
PT New human lung-specific polynucleotides and polypeptides for the
PT diagnosis and treatment of disease e.g. lung cancer.
XX
PS Example 6; Page 195; 378pp; English.
XX
CC The invention relates to isolated lung tumour-specific proteins and their
CC corresponding cDNA molecules. Lung tumour-specific proteins and their
CC antigen-presenting cells are useful for stimulating and/or expanding T
CC cells specific for a tumour protein, and for inhibiting the development
CC of cancer. The invention also relates to a composition useful for
CC stimulating an immune response, and for treating cancer. The lung tumour
CC specific oligonucleotide is useful in gene therapy and for diagnosis,
CC detection and treatment of lung cancer. The present sequence is human
CC lung tumour-specific protein
XX
SQ Sequence 133 AA;

Query Match      67.9%; Score 473; DB 4; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MNHTSQAFITAASGGQPPNYRIKEEYEAEMGAPHSASVRTTVINMPREVSVPDHVW 60
Db      1 MNHTVQTFPSVNSGGQPPNYEMLKEHEVAVLGAPHPAPTSTVIHIRSTSVDPHVW 60

Qy      61 SLFNTLFMNPCCGLGFIAPFAISVKSRRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Db      61 SLFNTLFMNPCCGLGFIAPFAISVKSRRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
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Qy      121 TIVSVIII 128
Db      121 LIVIPVLI 128

RESULT 10
ABR41053
ID ABR41053 standard; protein; 133 AA.
XX
AC ABR41053;
XX
DT 22-MAY-2003 (first entry)
XX
DE Human MAP kinase cascade activator #38.
XX
KW Human; Elk1 phosphorylation; Elk1 phosphorylation kinase; virucide;
KW antiinflammatory; immunomodulator; cytostatic; antiallergic; anti-HIV;
KW antirheumatic; antiarthritic; antidiabetic; antiasthmatic; gene therapy;
KW inflammation; autoimmune disease; viral disease; cancer; diabetes;
KW rheumatoid arthritis; asthma; allergic rhinitis; AIDS; viral hepatitis;
KW IgA nephritis.
XX
OS Homo sapiens.
XX
PN WO2003008589-A1.
XX
PD 30-JAN-2003.
XX
PF 15-JUL-2002; 2002WO-JP007174.
XX
PR 18-JUL-2001; 2001JP-00218204.
XX
PR 31-AUG-2001; 2001JP-00263450.
XX
PR 21-JAN-2002; 2002JP-00012176.
XX
PA (ASAH ) ASAH KASEI KOGYO KK.
XX
PI Matsuzaki O, Matsuda A, Nagano Y, Suzuki N;
XX
DR WPI; 2003-229582/22.
XX
DR N-PSDB; ACC42319.
XX
PT Elk1 phosphorylation-associated gene and its encoded protein with MAP
PT kinase cascade effect, applicable in diagnosis of and developing drugs
PT for e.g. inflammations, autoimmune diseases, viral diseases and cancer.
XX
PS Claim 1; Page 290; 762pp; Japanese.
XX
CC The invention relates to a novel purified protein having Elk1
CC phosphorylation activity and/or an activity of activating Elk1
CC phosphorylation kinase. A protein of the invention has antiinflammatory,
CC immunomodulator, virucide, cytostatic, antiallergic, antirheumatic,
CC antiarthritic, antidiabetic, antiasthmatic, and anti-HIV activity. The
CC polynucleotides may have a use in gene therapy. The gene and its encoded
CC protein are applicable in diagnosis of and developing drugs for e.g.
CC inflammations, autoimmune diseases, viral diseases and cancer such as
CC rheumatoid arthritis, diabetes; asthma, allergic rhinitis, AIDS, viral
CC hepatitis and IgA nephritis. The present sequence is used in the
CC exemplification of the invention
XX
SQ Sequence 133 AA;

Query Match      67.9%; Score 473; DB 6; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

Qy      1 MNHTSQAFITAASGGQPPNYRIKEEYEAEMGAPHSASVRTTVINMPREVSVPDHVW 60
Db      1 MNHTVQTFPSVNSGGQPPNYEMLKEHEVAVLGAPHPAPTSTVIHIRSTSVDPHVW 60

Qy      61 SLFNTLFMNPCCGLGFIAPFAISVKSRRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
Db      61 SLFNTLFMNPCCGLGFIAPFAISVKSRRKMGVDVTGAQAYASTAKCLNIWALILGILMTIL 120
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QY 121 TIVSVIII 128
DB 121 LIVIPVLI 128

RESULT 11
ADD66432
ID ADD66432 standard; protein; 133 AA.
AC ADD66432;
DT 15-JAN-2004 (first entry)
XX Human lung tumour-specific related protein, SEQ ID No 124.
DE expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
KW human; lung tumour-specific.
XX Homo sapiens.
OS WO200292001-A2.
PN 21-NOV-2002.
PD 10-MAY-2002; 2002WO-US014975.
XX 11-MAY-2001; 2001US-00854133.
PR (CORI-) CORIXA CORP.
PA Lodes MJ, Wang T, Fan L, Algate PA, Mcneill PD;
XX WPI; 2003-120592/11.
DR New polynucleotide and polypeptide, useful for preparing a composition
PT for diagnosing, treating or preventing cancer.
XX Disclosure; SEQ ID NO 124; 494pp; English.
XX The invention relates to a novel isolated polynucleotide comprising one
CC of 32 47-6080 base pair sequences, given in the specification, or their
CC complements or degenerate variants, at least 20 contiguous residues of a
CC sequence in, or having at least 75 or 90 % identity with the isolated
CC polynucleotide, or that hybridise with the polynucleotide. The invention
CC further comprises: an isolated polypeptide; an expression vector
CC comprising the polynucleotide operably linked to an expression control
CC sequence; a host cell transformed or transfected with the expression
CC vector; an isolated antibody or its antigen-binding fragment that
CC specifically binds to the polypeptide; a method for detecting the
CC presence of a cancer in a patient; a fusion protein comprising the
CC polypeptide; an oligonucleotide that hybridises to the isolated
CC polynucleotide under moderately stringent conditions; a method for
CC stimulating and/or expanding T cells specific for a tumour protein; an
CC isolated T cell population; a composition comprising a first component
CC consisting of carriers and immunostimulants and a second component; a
CC method for stimulating an immune response in a patient; a method for
CC treating cancer in a patient; a method for determining cancer in a
CC patient; a diagnostic kit comprising at least one oligonucleotide or
CC antibody and a detection reagent comprising a reporter group; and a
CC method for inhibiting the development of cancer in a patient. The
CC compositions of the invention have cytostatic activity and can be used to
CC create a vaccine. The isolated polynucleotide is useful for preparing a
CC composition for diagnosing, treating or preventing cancer. This sequence
CC represents a human lung tumour-specific protein relating to the
CC invention.
XX Sequence 133 AA;
QY Query Match 67.9%; Score 473; DB 7; Length 133;
Best Local Similarity 70.3%; Pred No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
QY 1 MNHTSQAFITAGGQPPNYERIKEEYEYAEVAGPHASVRRVTVINMPREVSPDHYVW 60
DB 1 MNHTVQTFFSPVNSQPPNYENMLKEEHEVAVLGAPHNPAPTSTVIHIRSTSVDPHYVW 60
QY 61 SLFNTLFNFFCCLGFIAYAYSVKSRDRKMGVDVTCGAQAYASTAKCLNISTVLSTLMVVI 120
DB 61 SLFNTLFNFFCCLGFIAYAYSVKSRDRKMGVDVTCGAQAYASTAKCLNISTVLSTLMVVI 120
QY 121 TIVSVIII 128
DB 121 LIVIPVLI 128

RESULT 12
ADE63839
ID ADE63839 standard; protein; 133 AA.
XX AC ADE63839;
XX 29-JAN-2004 (first entry)
DT Human Protein Q01628, SEQ ID NO 9783.
DE Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX Homo sapiens.
OS WO2003016475-A2.
PN 27-FEB-2003.
PD 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
PI WPI; 2003-268312/26.
DR GENBANK; Q01628.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
```

CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 133 AA;

Query Match 67.9%; Score 473; DB 7; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVRTTVINMPREVSVDPDHVW 60
DB 1 MNHTVQTFSPVNSGQPPNYEMLEKEHEVAVLGAPHNPAPTSTVHIRSETSVDPDHVW 60
QY 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTVLISILMVVI 120
DB 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALIIGILMTIL 120

QY 121 TIVSVIII 128
DB 121 LIVIPVLI 128

RESULT 13
ADD46417
ID ADD46417 standard; protein; 133 AA.

XX ADD46417;

DT 29-JAN-2004 (first entry)

XX Human Protein Q01628, SEQ ID NO 12097.

XX Human; pain; neuronal tissue; Gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

XX (FARB) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

XX WPI; 2003-269312/26.

XX GENBANK; Q01628.

XX New composition comprising two or more isolated polypeptides, useful for

XX preparing a medicament for treating pain in an animal.

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
CC human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 133 AA;

Query Match 67.9%; Score 473; DB 7; Length 133;
Best Local Similarity 70.3%; Pred. No. 6.9e-51;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAAAGGQPPNYERIKEEYEVAEMGAPHGASVRTTVINMPREVSVDPDHVW 60
DB 1 MNHTVQTFSPVNSGQPPNYEMLEKEHEVAVLGAPHNPAPTSTVHIRSETSVDPDHVW 60

QY 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTVLISILMVVI 120
DB 61 SLFNTLFMNFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNIWALIIGILMTIL 120

QY 121 TIVSVIII 128

DB 121 LIVIPVLI 128

RESULT 14
ADE87686

ID ADE87686 standard; protein; 133 AA.

XX ADE87686;

DT 29-JAN-2004 (first entry)

XX Human lung tumour antigen polypeptide #50.

XX Human; lung tumour antigen; cancer; lung cancer; CD4+; CD8+; T cell;
KW immune response; immunostimulant; cytostatic.

XX Homo sapiens.

XX US2003118599-A1.

XX 26-JUN-2003.

XX 10-MAY-2002; 2002US-00144649.

XX 02-APR-1999; 99US-00285323.

PR 03-AUG-1999; 99US-00370838.

PR 30-DEC-1999; 99US-00476235.

PR 03-MAR-2000; 2000US-00518809.

PR 29-MAR-2000; 2000US-00538037.

PR 05-JUN-2000; 2000US-00588937.

PR 18-AUG-2000; 2000US-00640878.

PR 20-SEP-2000; 2000US-00667170.

PR 01-NOV-2000; 2000US-00704512.

PR 14-DEC-2000; 2000US-00738973.

PR 11-MAY-2001; 2001US-00854133.

XX (CORI-) CORIXA CORP.

XX

PI Algate PA, Lodes MJ, Wang T, Fan L, McNeill PD;
 XX WPI; 2003-897103/82.
 XX N-PSDB; ADB87681.
 XX
 PT New polynucleotides encode lung tumor antigens and are useful to
 PT stimulate an immune response or detect or treat a cancer in a patient,
 PT particularly lung cancer.
 XX
 XX Example 6; SEQ ID NO 124; 63pp; English.
 XX
 CC The invention relates to polynucleotides encoding lung tumour antigens.
 CC The invention also relates to the polypeptides encoded by the
 CC polynucleotides, isolated antibodies or antigen-binding fragments that
 CC specifically bind the polypeptides and a method for detecting cancer in a
 CC patient, comprising obtaining a biological sample from the patient,
 CC contacting the sample with a binding agent that binds a polypeptide of
 CC the invention, detecting in the sample an amount of polypeptide that
 CC binds to the binding agent, and comparing the amount of polypeptide to a
 CC predetermined cut-off value. T cells specific for a tumour protein can be
 CC stimulated and/or expanded by contacting the T cells with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide. Cancer development can be inhibited by incubating CD4+
 CC and/or CD8+ T cells isolated from a patient with a polypeptide,
 CC polynucleotide or an antigen-presenting cell that expresses a
 CC polypeptide, so that the T cells proliferate. The invention is used to
 CC stimulate an immune response or to detect or treat a cancer in a patient,
 CC particularly lung cancer. This sequence represents a human lung tumour
 CC antigen polypeptide of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification but was obtained in
 CC electronic format from USPTO at seqdata.uspto.gov/sequence.html.
 XX
 XX Sequence 133 AA;

Query Match 67.9%; Score 473; DB 7; Length 133;
 Best Local Similarity 70.3%; Pred. No. 6.9e-51;
 Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHSASVRTTINNPREVSDPDHVVW 60
 DB 1 MNHTVQTFFSPVNSGQPPNYEMLEKEHEVAVLGAPHPNPAPTSTVIHRSSTVSDPDHVVW 60
 QY 61 SLFNTLFMNFCCGLGFIAVAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
 DB 61 SLFNTLFMNFCCGLGFIAFAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
 QY 121 TIVSVIII 128
 DB 121 LIVIPVLI 128

RESULT 15
 ABP43105
 ID ABP43105 standard; protein; 143 AA.
 XX
 AC ABP43105;
 XX
 DT 22-AUG-2002 (first entry)
 XX
 DE Human ovarian antigen HVCBB19, SEQ ID NO:4237.
 XX
 KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.

XX WO200200677-A1.
 XX 03-JAN-2002.
 XX
 PF 07-JUN-2001; 2001WO-US018569.
 XX
 PR 07-JUN-2000; 2000US-0209467P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Birse CE, Rosen CA;
 XX WPI; 2002-147878/19.
 DR N-PSDB; ABQ56182.
 XX
 PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 PS
 XX Claim 11; SEQ ID NO 4237; 2922pp; English.
 XX
 CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use
 CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovarian and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 143 AA;

Query Match 67.9%; Score 473; DB 5; Length 143;
 Best Local Similarity 70.3%; Pred. No. 7.6e-51;
 Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
 QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHSASVRTTINNPREVSDPDHVVW 60
 DB 11 MNHTVQTFFSPVNSGQPPNYEMLEKEHEVAVLGAPHPNPAPTSTVIHRSSTVSDPDHVVW 70
 QY 61 SLFNTLFMNFCCGLGFIAVAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
 DB 71 SLFNTLFMNFCCGLGFIAFAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 130
 QY 121 TIVSVIII 128
 DB 131 LIVIPVLI 138

Search completed: June 18, 2005, 16:31:42

Job time : 164 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 18, 2005, 16:17:44 ; Search time 177 Seconds
(without alignments)
396.355 Million cell updates/sec

Title: US-10-621-911A-2
Perfect score: 697
Sequence: 1 MNHRSQAFITRAGSGQPPNY.....VVITIVSVIIIVLNAQNLIHT 137

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	697	100.0	137	Q9CQW9	m mus muscu
2	693	99.4	137	Q9D8L6	mus musculus
3	646	92.7	137	INIB RAT	rattus norv
4	497.5	71.4	144	Q9R175	rattus norv
5	497	71.3	144	Q9S793	mus musculus
6	473	67.9	133	1 IFN3_HUMAN	homo sapien
7	454	65.1	132	Q6F8H2	homo sapien
8	452	64.8	146	Q9SMQ3	bos taurus
9	449	64.4	132	1 IFM2_HUMAN	homo sapien
10	427	61.3	93	Q9R176	rattus norv
11	388.5	55.7	107	Q9D3R8	mus musculus
12	388.5	55.7	113	Q8BVR2	mus musculus
13	385.5	55.3	106	Q9D103	mus musculus
14	385.5	55.3	106	Q8R2S7	mus musculus
15	384.5	55.2	125	1 IFM1_HUMAN	homo sapien
16	378.5	54.3	125	Q9SMQ2	bos taurus
17	268.5	38.5	152	Q7S7S1	xenopus lae
18	266	38.2	152	Q14617	homo sapien
19	225	32.3	107	1 I14K_TORMA	torpedo mar
20	210	30.1	128	Q8QFL3	oncorhynch
21	203	29.1	127	Q8QFM4	oncorhynch
22	194.5	27.9	130	Q810P6	mus musculus
23	191.5	27.5	134	Q88728	mus musculus
24	155.5	22.3	92	Q8UH61	ictalurus p
25	129.5	18.6	162	Q8BR26	mus musculus
26	109.5	15.7	340	Q96FA8	homo sapien
27	109.5	15.7	340	Q7Z6L0	homo sapien
28	109.5	15.7	394	Q8N2N8	homo sapien
29	108	15.5	341	Q8ND36	homo sapien
30	100.5	14.4	111	Q8PQ26	xanthomonas
31	96.5	13.8	114	Q8PD53	xanthomonas

32	96	13.8	179	2	Q6DFT4	Q6dft4 xenopus tro
33	86.5	12.4	169	2	Q9NC83	Q9nc83 strongyloce
34	83.5	12.0	688	2	Q950Y4	Q950y4 tetrahymena
35	83.5	12.0	688	2	Q9T7M6	Q9t7m6 tetrahymena
36	83.5	12.0	698	1	COX1_TETPY	P11947 tetrahymena
37	83	11.9	173	2	Q8C838	Q8c838 mus musculus
38	83	11.9	722	2	Q8Y3Q8	Q8y3q8 listeria mo
39	82.5	11.8	722	2	Q71VY5	Q71vy5 listeria mo
40	80	11.5	110	2	Q73T16	Q73t16 mycobacteri
41	80	11.5	645	1	COX1_PARTB	P05489 paramecium
42	79.5	11.4	257	2	Q8HQE2	Q8hq82 schizosacch
43	78	11.2	258	1	CT39_HUMAN	Q9h7v2 homo sapien
44	78	11.2	324	2	Q67ER8	Q67er8 rattus norv
45	77.5	11.1	254	2	Q88Y29	Q88y29 lactobacilli

ALIGNMENTS

RESULT 1
Q9CQW9 ID Q9CQW9 PRELIMINARY; PRT; 137 AA.
AC Q9CQW9;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched
DE library, clone:1810061A10 product:INTERFERON-INDUCIBLE PROTEIN homolog
DE (Mus musculus 18-day embryo whole body cDNA, RIKEN full-length
DE enriched library, clone:111004C05 product:INTERFERON-INDUCIBLE
DE PROTEIN homolog) (Fragilis) (interferon-inducible protein 15)
DE (Interferon induced transmembrane protein 3).
GN Name=Ifitm3;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;
EX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;
EX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;
EX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;
EX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas, and Whole body;
EX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,


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[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kikunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujikawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
[6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiracka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK007916; BAB25347.1; -.
DR MGD; MGI:1913391; Ifitm3.
DR GO; GO:0016023; C:cytoplasmic vesicle; IDA.
DR GO; GO:0008285; P:negative regulation of cell proliferation; IDA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 137 AA; 1498 MW; C9BED26B38D351P CRC64;

Query Match          99.4%; Score 693; DB 2; Length 137;
Best Local Similarity 99.3%; Pred. No. 9.1e-65;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTTTINNPREVSDPHVW 60
DB 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTTTINNPREVSDPHVW 60
QY 61 SLFNTLFNMFCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNSTLVLSTLMVVI 120
DB 61 SLFNTLFNMFCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNSTLVLSTLMVVI 120
QY 121 TIVSVIIIVLNAQNLT 137
DB 121 TIVSVIIIVLNAQNLT 137

RESULT 3
INIB RAT
ID INIB RAT STANDARD; PRT; 137 AA.
AC P26376;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Interferon-inducible protein.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Hayzer D.J.;
RL Submitted (AUG-1991) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- INDUCTION: By interferon beta.
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein

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family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X61381; CAA43655.1; -.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Interferon induction; Transmembrane.
FT TRANSMEM 58 78 Potential.
FT TRANSMEM 110 130 Potential.
SQ SEQUENCE 137 AA; 14971 MW; 9D3F92264E0C0FC2 CRC64;

Query Match          92.7%; Score 646; DB 1; Length 137;
Best Local Similarity 89.8%; Pred. No. 8e-60;
Matches 123; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTTTINNPREVSDPHVW 60
DB 1 MNHTSQAFITAAAGCGPPNYERIKEEYEVAEMGAPHGASVTTTINNPREVSDPHVW 60
QY 61 SLFNTLFNMFCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNSTLVLSTLMVVI 120
DB 61 SLFNTLFNMFCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNSTLVLSTLMVVI 120
QY 121 TIVSVIIIVLNAQNLT 137
DB 121 TIVSVIIIVLNAQNLT 137

RESULT 4
Q9R175
ID Q9R175 PRELIMINARY; PRT; 144 AA.
AC Q9R175;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Interferon-inducible protein 16 (Hypothetical protein).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22531601; PubMed=12644301; DOI=10.1016/S0303-7207(02)00412-4;
RA Daido H., Zhou M.Y., Gomez-Sanchez E.P., Gomez-Sanchez C.E.;
RT "Interferon-inducible genes in the rat adrenal gland and vascular
RL smooth muscle cells.";
RL Mol. Cell. Endocrinol. 200:81-87 (2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting J., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

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RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Pituitary gland;
RA Strausberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF164040; AAD48011.1; -.
DR EMBL; BC060563; AAH60563.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Hypothetical protein.
SQ SEQUENCE 144 AA; 5F7AA11F655D2DAB CRC64;
      71.4%; Score 497.5; DB 2; Length 144;
Query Match 69.2%; Pred. No. 3.4e-44;
Best Local Similarity 16; Mismatches 21; Indels 7; Gaps 2;
Matches 99; Conservative 16; Mismatches 21; Indels 7; Gaps 2;
QY 1 MNHTSOAFITAAAGCGPPNYVERIKEEYEVAEMGAPHGSAVTRTTVINMPREVSVPDHHVW 60
DB 1 MSHNSQAFI-L-PAAGLPPSYETIKEEYGVTELGPNSAVVTRTTVINMPREVSVPDHHVW 59
QY 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
DB 60 SLFNTLFFNACCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVII 119
QY 121 TIV-----SVIIIVNAQLHT 137
DB 120 CIIIFSTTSVAVFOSLSQRTPHS 142
RESULT 5
Q99J93 ID Q99J93 PRELIMINARY; PRT; 144 AA.
AC Q99J93;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Ifitm2 protein (Interferon induced transmembrane protein 2) (Fragilis
DE R).
GN Name=ifitm2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Vallalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=mix FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvEv;
RA Saitou M., Barton S., Surani M.A.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002160; AAH02160.1; -.
DR EMBL; BC002102; AAH02102.1; -.
DR EMBL; AY082486; AAM03318.1; -.
DR MGD; MGI:1933382; Ifitm2.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Transmembrane.
SQ SEQUENCE 144 AA; 15743 MW; 99C7CDBA25CAFI9A9 CRC64;
      71.3%; Score 497; DB 2; Length 144;
Query Match 71.7%; Pred. No. 3.9e-44;
Best Local Similarity 13; Mismatches 20; Indels 6; Gaps 2;
Matches 99; Conservative 13; Mismatches 20; Indels 6; Gaps 2;
QY 1 MNHTSOAFITAAAGCGPPNYVERIKEEYEVAEMGAPHGSAVTRTTVINMPREVSVPDHHVW 60
DB 1 MSHNSQAFI-L-STNAGLPPSYETIKEEYGVTELGPNSAVVTRTTVINMPREVSVPDHHVW 59
QY 61 SLFNTLFMNFCCGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
DB 60 SLFNTLFFNACCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVII 119
QY 121 TIV-----SVIIIVNAQ 133
DB 120 CIIIFSTTSVAVFQSPAQ 137
RESULT 6
IFM3_HUMAN ID IFM3_HUMAN STANDARD; PRT; 133 AA.
AC Q01628; Q96HK8; Q96J15;
DT 01-JUL-1993 (Rel. 26, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Interferon-induced transmembrane protein 3 (Interferon-inducible
DE protein 1-8U).
GN Name=IFITM3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cervix;
RX MEDLINE=91301153; PubMed=1906403;
RA Lewin A.R., Reid L.E., McMahon M., Stark G.R., Kerr I.M.;
RT "Molecular analysis of a human interferon-inducible gene family.";
RL Eur. J. Biochem. 199:417-423(1991).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Cervix;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Vallalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
```

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- INDUCTION: By alpha and gamma interferons.
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein
CC family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X57352; CAA40626.1; -;
DR EMBL; BC006794; AAH06794.1; -;
DR EMBL; BC008417; AAH08417.1; -;
DR EMBL; BC022439; AAH22439.1; -;
DR PIR; S17182; S17182.
DR Genew; HGNC:5414; IFITM3.
DR H-InvDB; HIX0021368; -;
DR MIM; 605579; -;
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
KW Interferon induction; Transmembrane.
FT TRANSMEM 58 78 Potential.
FT TRANSMEM 108 128 Potential.
FT CONFLICT 2 2 N -> S (in Ref. 1).
FT CONFLICT 3 3 H -> Q (in Ref. 2); AAH08417/AAH22439).
FT CONFLICT 34 34 A -> G (in Ref. 1).
SQ SEQUENCE 133 AA; 14632 MW; 9FFB2B4623F7A1DD CRC64;
Query Match 67.9%; Score 473; DB 1; Length 133;
Best Local Similarity 70.3%; Pred. No. 1.2e-41;
Matches 90; Conservative 14; Mismatches 24; Indels 0; Gaps 0;
Qy 1 MNHTSQAFITTAASGQPPNYERIKEEYEVAEMGAPHGASVVRTTINNMPREVSVPDHYVW 60
Db 1 MNHTVQTFSPVNSGQPPNYEMLKEEHEVAVLGAPHPAPPTSTVIHRSSTVDPDHYVW 60
Qy 61 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 61 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Qy 121 TIVSVIII 128
Db 121 LIVPVLII 128
RESULT 7
Q6FH82 PRELIMINARY; PRT; 132 AA.
AC Q6FH82;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IFITM2 protein (Fragment).
GN Name=IFITM2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
RA Neubert P., Ketrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., LaBaer J.,
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR541874; CAG46672.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
FT NON_TER 132 132
SQ SEQUENCE 132 AA; 14604 MW; 2B9B09CFF7E05FB3 CRC64;
Query Match 65.1%; Score 454; DB 2; Length 132;
Best Local Similarity 66.9%; Pred. No. 1.2e-39;
Matches 89; Conservative 16; Mismatches 26; Indels 2; Gaps 2;
Qy 1 MNHTSQAFITTAASGQPPNYERIKEEYEVAEMGAPHGASVVRTTINNMPREVSVPDHYVW 60
Db 1 MNHTVQTF-SPVNSGQPPNYEMLKEEHEVAVLGAPHPAPPTSTVIHRSSTVDPDHYVW 59
Qy 61 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 60 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 119
Qy 121 TIVSVIII 133
Db 120 LII-IPVLVQAQ 131
RESULT 8
Q95MQ3 PRELIMINARY; PRT; 146 AA.
AC Q95MQ3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Interferon-induced protein 1-8U.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21526490; PubMed=11673264;
RT Pru J.K., Austin K.J., Haas A.L., Hansen T.R.;
RT "Pregnancy and interferon-tau upregulate gene expression of members of
RT the 1-8 family in the bovine uterus.";
RL Biol. Reprod. 65:1471-1480(2001).
DR EMBL; AF272041; AAK58638.1; -;
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 146 AA; 15723 MW; E8A6FC3E5A7FB19D CRC64;
Query Match 64.8%; Score 452; DB 2; Length 146;
Best Local Similarity 67.2%; Pred. No. 2.1e-39;
Matches 84; Conservative 18; Mismatches 23; Indels 0; Gaps 0;
Qy 1 MNHTSQAFITTAASGQPPNYERIKEEYEVAEMGAPHGASVVRTTINNMPREVSVPDHYVW 60
Db 1 MNRTSQLLLTGAGVAPPAYEVLKEEHEVAVLGAPQSQAPLTTTINIRSDTAVPDHYVW 60
Qy 61 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Db 61 SLFNTLFNMFCCLGFIAYAYSVKSRDRKMGVDVTGAQAYASTAKCLNISTLVLSILMVVI 120
Qy 121 TIVSV 125
Db 121 LIVLV 125

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RESULT 9
IFM2_HUMAN
ID Q91629; Q96DA8; STANDARD; PRT; 132 AA.
AC Q91629; Q96DA8;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Interferon-induced transmembrane protein 2 (Interferon-inducible
DE protein 1-8D).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=91301153; PubMed=1906403;
RA Lewin A.R., Reid L.E., McMahon M., Stark G.R., Kerr I.M.;
RT "Molecular analysis of a human interferon-inducible gene family.";
RL Eur. J. Biochem. 199;417-423(1991).
RN [2]
SEQUENCE FROM N.A.
RP TSSUB=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Shat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J.,
RA Bonak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99;16899-16903(2002).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- INDUCTION: By alpha and gamma interferons.
CC -!- SIMILARITY: Belongs to the IFN-induced transmembrane protein
CC family.
CC -----
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CC -----
CC EMBL; X57351; CAA0625.1; -.
CC EMBL; BC009696; AAH09696.1; -.
CC PIR; S17183; S17183.
CC Genew; HGNC:5413; IFITM2.
CC MIM; 605578; -.
CC GO; GO:0006955; P:immune response; TAS.
CC InterPro; IPR007593; CD225.
CC Pfam; PF04505; CD225; 1.
CC Interferon induction; Polymorphism; Transmembrane.
FT TRANSMEM 57 77 Potential.
FT VARIANT 41 41 T -> M (in dbSNP:14408).
FT 41 41 G -> A (in Ref. 2).
FT CONFLICT 33 33
FT SEQUENCE 132 AA; 14546 MW; D42F47CA225D3465 CRC64;
SQ
Query Match 64.4%; Score 449; DB 1; Length 132;
Best Local Similarity 65.4%; Pred. No. 3.9e-39;
Matches 87; Conservative 17; Mismatches 27; Indels 2; Gaps 2;
QY 1 MNHTSQAFITAAASGGOPPNYRIKEEYVAEMGAPHSASVTRTTVINMPREVSVPDHVW 60
DB 1 MNHIVQTF-SPVNSGGOPPNYEMLEKEQEVAMLGPPHPAPPTSTVIHIRSTVDPDHVW 59
QY 61 SLNTFLFMNFCCLGFTIAYAYSVKSRDRKMWGDVTGAQAYASTAKCLINISLVLISILMWVI 120
DB 60 SLNTFLFMNFCCLGFTIAYAYSVKSRDRKMWGDVTGAQAYASTAKCLINISLVLISILMWVI 119
QY 121 TIVSVIIIVLNAQ 133
DB 120 LVI-IPVLVVOAQ 131
RESULT 10
Q9R176 PRELIMINARY; PRT; 93 AA.
AC Q9R176;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Interferon-inducible protein variant 10.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=22531601; PubMed=12644301; DOI=10.1016/S0303-7207(02)00412-4;
RA Daido H., Zhou M.Y., Gomez-Sanchez E.P., Gomez-Sanchez C.E.;
RT "Interferon-inducible genes in the rat adrenal gland and vascular
RT smooth muscle cells.";
RL Mol. Cell. Endocrinol. 200;81-87(2003).
DR EMBL; AF164039; AAD48010.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009607; P:response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 93 AA; 10241 MW; 98130648468A9215 CRC64;
Query Match 61.3%; Score 427; DB 2; Length 93;
Best Local Similarity 94.0%; Pred. No. 5.5e-37;
Matches 78; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNHTSQAFITAAASGGOPPNYRIKEEYVAEMGAPHSASVTRTTVINMPREVSVPDHVW 60
DB 1 MNHTSQAFVNAATGGOPPNYRIKEEYVSELGAPHSASVTRTTVINMPREVSVPDHVW 60
QY 61 SLNTFLFMNFCCLGFTIAYAYSVK 83
DB 61 SLNTFLFMNFCCLGFTIAYAYSVK 83
RESULT 11
Q9D3R8 PRELIMINARY; PRT; 107 AA.
AC Q9D3R8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male testis cDNA, RIKEN full-length enriched
DE library, clone:4933438K12 product:similar to INTERFERON-INDUCIBLE
DE PROTEIN.
GN Name=ifitm7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP
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Qy	84	SRDRKVVGDVTGAQYASTAKCNLTINSLVLSILMVVITI	122
Db	62	SRDRKVVGDVTGAQYASTARCLNTSCLTSLVVMVILFI	100

RESULT 12

Q8BVR2	PRELIMINARY;	PRT;	113 AA.
ID	Q8BVR2		
AC	Q8BVR2;		
DT	01-MAR-2003 (TrEMBLrel. 23, Created)		
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)		
DT	01-JUN-2003 (TrEMBLrel. 24, Last annotation update)		
DE	Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930507H06 product:similar to INTERFERON-INDUCIBLE PROTEIN.		
DE	DE		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;		
RC	Carninci P., Hayashizaki Y.;		
RC	"High-efficiency full-length cDNA cloning.";		
RC	Meth. Enzymol. 303:19-44(1999).		
RN	[2]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;		
RC	RIKEN FANTOM Consortium;		
RC	"Functional annotation of a full-length mouse cDNA collection.";		
RC	Nature 409:685-690(2001).		
RN	[3]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	The FANTOM Consortium;		
RC	the RIKEN Genome Exploration Research Group Phase I & II Team;		
RC	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";		
RC	Nature 420:563-573(2002).		
RN	[4]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;		
RC	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,		
RC	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;		
RC	"Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."		
RC	Genome Res. 10:1617-1630(2000).		
RN	[5]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	MEDLINE=20530913; PubMed=11076961; DOI=10.1101/gr.152600;		
RC	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,		
RC	Konno H., Akiyama J., Nishi K., Kikunai T., Teshiro H., Itoh M.,		
RC	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,		
RC	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,		
RC	Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,		
RC	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,		
RC	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;		
RC	"RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer.";		
RC	Genome Res. 10:1757-1771(2000).		
RN	[6]		
SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Testis;		
RC	Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,		
RC	Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,		
RC	Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,		
RC	Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,		
RC	Ra Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Koyda M., Koya S.,		

KN		SEQUENCE FROM N.A.
RN	[6]	STRAIN=C57BL/6J; TISSUE=Testis;
RC		Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA		Adachi J., Aizawa K., Akimura T., Hara A., Hashizume W.,
RA		Fukuda S., Furuno M., Hanagaki T., Hiraoka T., Hirozane T.,
RA		Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hizekawa T.,
RA		Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA		Kato H., Kawai J., Kohjima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA		Katoh H., Kawai J., Kohjima Y., Kondo S., Konno H., Kouda M., Koya S.,

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RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito K., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RA Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK076846; BAC36505.1; -.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR GO; GO:0009607; P: response to biotic stimulus; IEA.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 113 AA; 12679 MW; A016A02PB57B3310 CRC64;

Query Match 55.7%; Score 388.5; DB 2; Length 113;
Best Local Similarity 73.7%; Pred. No. 7.6e-33;
Matches 73; Conservative 14; Mismatches 11; Indels 1; Gaps 1;

QY 24 KEEYEVAEMGAPHGASASVTRTTVIMPREVSPDHVWVSLFTLPMNFCCLGFTAYAYSVK 83
DB 3 KQHEVVVMTGPHSTSTTTIITMP-EISKPDVWVWVSLFTLPMNFCCLGFTAYAYSVK 61

QY 84 SRDRKMWGDTGTAQAYASTAKCLNISTLVLSILMVITV 122
DB 62 SRDRKMWGDTGTAQAFASATACLNISCLLSVWVILFI 100

RESULT 13
ID Q9D103 PRELIMINARY; PRT; 106 AA.
AC Q9D103;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Mus musculus 18-day embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:1110036C17 product:similar to INTERFERON-INDUCIBLE
DE PROTEIN (Fragilis2).
GN Name=Ifitm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA The FANTOM Consortium.
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20493374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
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[5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
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DR EMBL; AK004121; BAB23181.1; -.
DR EMBL; BK001123; DAA01238.1; -.
DR MGD; MGI:1915963; Ifitm1.
DR GO; GO:0016021; C: integral to membrane; TAS.
DR InterPro; IPR007593; CD225.
DR Pfam; PF04505; CD225; 1.
SQ SEQUENCE 106 AA; 11524 MW; 7B0E7D8200D36631 CRC64;

Query Match 55.3%; Score 385.5; DB 2; Length 106;
Best Local Similarity 73.0%; Pred. No. 1.5e-32;
Matches 73; Conservative 10; Mismatches 16; Indels 1; Gaps 1;

QY 24 KEEYEVAEMGAPHGASASVTRTTVIMPREVSPDHVWVSLFTLPMNFCCLGFTAYAYSVK 83
DB 3 KQHEVVVMTGPHSTSTTTIITMP-EISTPDVWVWVSLFTLPMNFCCLGFTAYAYSVK 61

QY 84 SRDRKMWGDTGTAQAYASTAKCLNISTLVLSILMVITV 123
DB 62 SRDRKMWGDTGTAQAFASATACLNISCLLSVWVILFI 101

RESULT 14
ID Q9R2S7 PRELIMINARY; PRT; 106 AA.
AC Q9R2S7;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Interferon induced transmembrane protein 1.
GN Name=Ifitm1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Query Match 55.2%; Score 384.5; DB 1; Length 125;
Best Local Similarity 67.3%; Pred. No. 2.2e-32;
Matches 76; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

Query Match 55.2%; Score 384.5; DB 1; Length 125;
Best Local Similarity 67.3%; Pred. No. 2.2e-32;
Matches 76; Conservative 16; Mismatches 18; Indels 3; Gaps 1;

Qy 24 KEEYEVAEMGAPHSASVRTTVINMPREVSVPDHHVWSLENTLFMNFCCCLGFTIAYAYSVK 83
Db 3 KEEHEVAVLGAPPSTILPRSTVINIHSETSVDPDHHVWSLENTLFMNFCCCLGFTIAYAYSVK 62
Qy 84 SRDRKMWGDVTGAQAYASTAKCLNISTVLISILMWVITIVSVIIIVLNAQNLH 136
Db 63 SRDRKMWGDVTGAQAYASTAKCLNINWALILGILM---TIGFILLVFGSVTVY 112

Search completed: June 18, 2005, 16:34:45
Job time : 180 secs